

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
 Au-Young, Janice
 Goli, Surya K.
 Hillman, Jennifer.
 Zweiger, Gary B.
- (ii) TITLE OF THE INVENTION: A NOVEL TUMOR PROTEIN
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: U.S.
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0126 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE: Consensus

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00162597.093098

4-1-0400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Ala Gln Ala Gln Gly Leu Leu Glu Thr Glu Pro Leu Gln Gly
 1 5 10 15
 Thr Asp Glu Asp Ala Val Ala Ser Ala Asp Phe Ser Ser Met Leu Ser
 20 25 30
 Glu Glu Glu Lys Glu Glu Leu Lys Ala Glu Leu Val Gln Leu Glu Asp
 35 40 45
 Glu Ile Thr Thr Leu Arg Gln Val Leu Ser Ala Lys Glu Arg His Leu
 50 55 60
 Val Glu Ile Lys Gln Lys Leu Gly Met Asn Leu Met Asn Glu Leu Lys
 65 70 75 80
 Gln Asn Phe Ser Lys Ser Trp His Asp Met Gln Thr Thr Thr Ala Tyr
 85 90 95
 Lys Lys Thr His Glu Thr Leu Ser His Ala Gly Gln Lys Ala Thr Ala
 100 105 110
 Ala Phe Ser Asn Val Gly Thr Ala Ile Ser Lys Lys Phe Gly Asp Met
 115 120 125
 Ser Tyr Ser Ile Arg His Ser Ile Ser Met Pro Ala Met Arg Asn Ser
 130 135 140
 Pro Thr Phe Lys Ser Phe Glu Glu Arg Val Glu Thr Thr Val Thr Ser
 145 150 155 160
 Leu Lys Thr Lys Val Gly Gly Thr Asn Pro Asn Gly Gly Ser Phe Glu
 165 170 175
 Glu Val Leu Ser Ser Thr Ala His Ala Ser Ala Gln Ser Leu Ala Gly
 180 185 190
 Gly Ser Arg Arg Thr Lys Glu Glu Leu Gln Cys
 195 200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCCAGCTG CGTTCTGAGC CTGGGCGCAG CTACCATCTG CTCTGGGAAG CACCAGGGTG 60
 TCCCCGCCGC CCTCAGCTCG AAGTCAGCCA CCATGGAGGC GCAGGCACAA GGTTCGTTGG 120
 AGACTGAACC GTTGCAAGGA ACAGACGAAG ATGCAGTAGC CAGTGCTGAC TTCTCTAGCA 180
 TGCTCTCTGA GGAGGAAAAG GAAGAGTTAA AAGCAGAGTT AGTTCAGCTA GAAGACGAAA 240
 TTACAACACT ACGACAAGTT TTGTCTAGCGA AAGAAAAGGCA TCTAGTTGAG ATAAAACAAA 300
 AACTCGGCAT GAACCTGATG AATGAATTAA AACAGAACTT CAGCAAAAAGC TGGCATGACA 360
 TGCAGACTAC CACTGCCTAC AAGAAAACAC ATGAAACCTT GAGTCACGCA GGGCAAAAGG 420
 CAACTGCAGC TTTCAGCAAC GTTGAACGG CCATCAGCAA GAAGTTCGGA GACATGAGTT 480
 ACTCCATTCTG CCATTCCATA AGTATGCCTG CTATGAGGAA TTCTCCTACT TTCAAATCAT 540
 TTGAGGAGAG GGTTGAGACA ACTGTCACAA GCCTCAAGAC GAAAGTAGGC GGTACGAACC 600
 CTAATGGAGG CAGTTTTGAG GAGGTCCTCA GCTCCACGGC CCATGCCAGT GCCCAGAGCT 660
 TGGCAGGAGG CTCCCGGCGG ACCAAGGAGG AGGAGCTGCA GTGCTAAGTC CAGCCAGCGT 720

GCAGTGCATC CAGAAACCGG CCACTACCCA GCCCATCTNT GCCTGTGCTT ATCCAGATAA
GAAGACCAAA

780
790

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro
1 5 10 15
Tyr Phe Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe
20 25 30
Trp Lys Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys
35 40 45
Lys Met Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile
50 55 60
Tyr Asp Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp
65 70 75 80
Leu Ile Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu
85 90 95
Tyr Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile
100 105 110
Met Ser Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe
115 120 125
Asp Trp Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val
130 135 140
His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp
145 150 155 160
Leu Tyr His Asn Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser
165 170 175
Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu
180 185 190
Gly Ser Trp Ala Arg Leu Asp Ala Arg Ala Val Val Thr Gly Leu Leu
195 200 205
Ala Leu Lys His Phe Gly Pro Val Cys Arg Arg Cys Gln Cys Ala Leu
210 215 220
Leu Gly Leu Val Ser Gln Thr Leu Met Tyr Leu Phe Pro Ala Ser Leu
225 230 235 240
Gln Val Leu Val Lys
245

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
(B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTMGMKCGCG	GGCCCCCGCC	AGTCAGGTGG	GTGCCAGGCC	CTGGCCGTGG	CGAAAGAGCC	60
GGCGGAGGGA	GGACCCGCTC	CCGGAGACGC	CGCCTCGCGA	TCCCCGCGCG	GGCGGGACCG	120
GGCGGCCGGC	ATCATGACCC	TGTTTCACTT	CGGGAAGTGC	TTCGCTCTTG	CCTACTTCCC	180
CTACTTCATC	ACCTACAAGT	GCAGCGGCCT	GTCCGAGTAC	AACGCCTTCT	GGAAATGCGT	240
CCAGGCTGGA	GTCACCTACC	TCTTTGTCCA	ACTCTGCAAG	ATGCTGTTCT	TGGCCACTTT	300
CTTTCCCACC	TGGGAAGGCG	GCATCTATGA	CTTCATTGGG	GAGTTCATGA	AGGCCAGCGT	360
GGATGTGGCA	GACCTGATAG	GTCTAAACCT	TGTCATGTCC	CGGAATGCCG	GCAAGGGAGA	420
GTACAAGATC	ATGGTTGCTG	CCCTGGGCTG	GGCCACTGCT	GAGCTTATTA	TGTCCCGCTG	480
CATTCCCCTA	TGGGTCGGAG	CCCGGGGCAT	TGAGTTTGAC	TGGAAGTACA	TCCAGATGAG	540
CATAGACTCC	AACATCAGTC	TGGTCCATTA	CATCGTCGCG	TCTGCTCAGG	TCTGGATGAT	600
AACACGCTAT	GATCTGTACC	ACAACCTCCG	GCCAGCTGTC	CTTCTGCTGA	TGTTCTCAG	660
TGTCTACAAG	GCCTTTGTTA	TGGAGACCTT	CGTCCACCTC	TGCTCGCTGG	GCAGTTGGGC	720
ARCTCTAMTG	GCCCCAGCAG	TGGTAACGGG	GCTGCTGGCC	CTCAAGCACT	TTGGSCCTGT	780
ATGTCGSCGT	TGTCAATGTG	CACTYCTAGG	CTTGGTGTCT	CAGACATTGA	TGTACCTTTT	840
CCCTGCCTCA	CTCCAGTTT	TAGTGAAGTA	AACAGTATTT	GGAAAGTT		888

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: 790225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	Arg	Gly	Glu	Gln	Gly	Leu	Leu	Arg	Thr	Asp	Pro	Val	Pro	Glu
1				5					10					15	
Glu	Gly	Glu	Asp	Val	Ala	Ala	Thr	Ile	Ser	Ala	Thr	Glu	Thr	Leu	Ser
			20					25					30		
Glu	Glu	Glu	Gln	Glu	Glu	Leu	Arg	Arg	Glu	Leu	Ala	Lys	Val	Glu	Glu
			35				40					45			
Glu	Ile	Gln	Thr	Leu	Ser	Gln	Val	Leu	Ala	Ala	Lys	Glu	Lys	His	Leu
	50					55					60				
Ala	Glu	Ile	Lys	Arg	Lys	Leu	Gly	Ile	Asn	Ser	Leu	Gln	Glu	Leu	Lys
65					70				75					80	
Gln	Asn	Ile	Ala	Lys	Gly	Trp	Gln	Asp	Val	Thr	Ala	Thr	Ser	Ala	Tyr
			85					90					95		
Lys	Lys	Thr	Ser	Glu	Thr	Leu	Ser	Gln	Ala	Gly	Gln	Lys	Ala	Ser	Ala
			100					105					110		

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PF-0126 US

Ala Phe Ser Ser Val Gly Ser Val Ile Thr Lys Lys Leu Glu Asp Val
115 120 125
Lys Asn Ser Pro Thr Phe Lys Ser Phe Glu Glu Lys Val Glu Asn Leu
130 135 140
Lys Ser Lys Val Gly Gly Thr Lys Pro Ala Gly Gly Asp Phe Gly Glu
145 150 155 160
Val Leu Asn Ser Ala Ala Asn Ala Ser Ala Thr Thr Thr Glu Pro Leu
165 170 175
Pro Glu Lys Thr Gln Glu Ser Leu
180

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1072344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Pro Lys Gly Asn Lys Lys Pro Asn Glu Lys Lys Glu Glu Leu Glu
1 5 10 15
Lys Phe Ala Lys Glu Leu Gln Gly Ser Asp Ser Asp Glu Asp Ala Val
20 25 30
Val Ile Glu Gln Pro Thr Val Glu Pro Lys Leu Pro Gln Asn Asp Ser
35 40 45
Ser Ser Ser Asn Lys Ile Val Leu Ser Gln Ala Glu Lys Asp Leu Leu
50 55 60
Arg Thr Glu Leu Asp Lys Thr Glu Glu Glu Ile Ser Thr Leu Lys Gln
65 70 75 80
Val Leu Ser Ala Arg Gln Lys His Ala Ala Glu Leu Lys Arg Lys Leu
85 90 95
Gly Leu Thr Pro Phe Ser Glu Leu Ser Gln Asp Ile Asn Arg Ser Leu
100 105 110
Lys Thr Val Thr Asp Thr Asp Ala Cys Thr His Phe Ile Glu Ile Asn
115 120 125
Ile Gln Lys Lys Lys Lys Gln Ser Met Tyr Tyr Ile Lys Arg Leu Ser
130 135 140
Lys Asn Ile Gln Thr Val Pro Ile Leu Thr Ser Glu Lys Lys Arg Ile
145 150 155 160
Leu His Ala Phe Ile Val Leu Lys Lys Lys Ser Ser Ile Leu Lys Ser
165 170 175
Leu Leu Leu Trp Gln Gln Tyr Gln Lys Thr Ala Glu Val Ala Ala Ala
180 185 190
Thr Ser Asp Thr Val Lys Glu Lys Trp Asn Asp Met Arg Asn Ser Ser
195 200 205
Leu Phe Lys Ser Phe Glu Ser Lys Leu Gly Ser Ala Leu Asn Asn Ala
210 215 220
Lys Met Ala Ala Ser Thr Ser Ile Asp His Leu Ala Gly Ala Ala Arg
225 230 235 240

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Gly Pro Ser Gln Thr Gly Thr Pro Val Ala Glu Glu Ala Lys Pro Ile
245 250 255
Ser

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 470373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Phe Phe His Phe Ile Asn Cys Phe Ala Leu Ala Phe Ala Pro
1 5 10 15
Tyr Phe Ile Val Tyr Lys Tyr Ser Gly Ile Asn Glu Tyr Ser Ser Ile
20 25 30
Trp Lys Cys Ala Thr Ala Ser Gly Gly Tyr Leu Leu Thr Gln Leu Ala
35 40 45
Lys Leu Leu Ile Ile Ala Thr Phe Phe Pro Ala Leu Asp Ser Glu Gly
50 55 60
Phe Ser Ile Val Pro Glu Phe Leu Lys Ser Ser Ala Asp Ile Ile Asp
65 70 75 80
Val Ile Gly Leu His Leu Leu Met Thr Asn Phe Leu Ala Gly Lys Gly
85 90 95
Glu Val Arg Phe Val Val Gly Gly Leu Gly Trp Gly Phe Ala His Ser
100 105 110
Val Ala His Arg Leu Val Leu Leu Trp Val Gly Ala Arg Gly Thr Ala
115 120 125
Phe Thr Trp Arg Trp Val Gln Thr Ser Leu Asp Ser Ser Ala Asp Leu
130 135 140
Leu Val Ile Val Ser Leu Ala Cys Leu Thr Trp Met Ile Thr Arg Thr
145 150 155 160
Pro Asn Lys Phe Leu Val Ser Pro Ile Leu Ala Ile Thr Val Gln His
165 170 175
Thr Phe Ser Leu Tyr Gly Trp Ser Leu Leu Ala Phe Arg Phe Ala Tyr
180 185 190
Ser Ile Ala Thr Ala Ile Leu Thr Val Val Val Tyr Ser Ala Asn Arg
195 200 205
Thr Ala Ser Thr Arg Lys Asn Glu
210 215